```
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
```

OM protein - protein search, using sw model

August 10, 1999, 06:14:03; Search time 9.95 Seconds (without alignments) 488.658 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-208-619-1 911 1 MEEYAREPCPWRIVDDCGGA.....QLPPKDGTPAPGYFSYQQYH 172

Scoring table: BLOSUM62

77977 segs, 28268293 residues Searched:

SwissProt_37:* .. Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	cription	035092 rattus norv	homo sa	P39515 saccharomyc	P87130 schizosacch		Q12328 saccharomyc		q			mus m					P40144 oryctolagus			_	schizos	_	_		-					streptc					mus mus	б	27420 caenorh	44236 h	183.1	47624 e	8680	0401	32332 s	Q59570 mycobacteri
SUMMARIES	ID	IM17 RAT	Ļ	IM17 YEAST	IM17_SCHPO	IM22_SCHPO	IM22_YEAST	IM23_YEAST	NUJM_NEUCR	CYA5_RAT	KPYR_HUMAN	PIN5_MOUSE	GLYA_BORBU	Y058_MYCTU	DC11_DROME	BRELA	CYA5_RABIT	KPYR_CANFA	TCR_STRRM	ACCD_MYCTU	YAGC_SCHPO	HRPN_ERWCA	YAJR_ECOLI	HYIN_AGRRA	YBDA_ECOLI	PIN5_HUMAN	PUR8_STRLP	EPA2_HUMAN	KDPD_RATRA	TCMA_STRGA	VGLB_RHCM6	SUMT_PSEFL	KPYR_MOUSE	KPYR_RAT		ELS_CHICK	HS7C_CAEEL	YF14_HAEIN	MTRD_METIM	SAPC_ECOLI	ಶ	YM78_YEAST	PMT_YEAST	THT3_MYCTU
	cength DB				164 1																																							
æ	ery		7	4	37.7	S.	ď.	ä	•			•	•	•	•	•	•		•	•	8.2				•	•		•		٠	٠	•	•		•	٠		•	•		•	•		
	Score				343.5			\sim		98	83	Φ,	80.5	٠.	80	7	78.5	7	76.5	97	7	4	٠	m.	m.	73	^		72.5		• 1	۲.	71.5	ή.	Ή.	^	70.5		70	~	69.5	φ.	69	69
	Result No.	1	7	က	4	2	9	7	80	O	10	11	12	E :	14	15	16	17	or	Ė		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	Ç	42	43

121 121 SULT 2	Qy 61 QIGGSFAVWGGLFXTIDCGLVRLRGKEDPWNSITSGALTGAVLAARSGPLAMVGSAMMGG 120	QY 1 MEEYAREPCPWRIVDDCGGAFTMGVIGGGVFQAIKGFRNAPVGIRHRLRGSANAVRIRAP 60 	Query Match 77.3%; Score 704.5; DB 1; Length 171; Best Local Similarity 75.4%; Pred. No. 3.4e-57; Matches 129; Conservative 17; Mismatches 24; Indels 1; Gaps 1	EMBL; AB(PROTEIN J TRANSMEM TRANSMEM TRANSMEM SEQUENCE	• ທ 3∗	-1- SUBDITIONS PART OF THE RECEPTOR COMPLEX THAT CONSIS LEAST 3 DIFFERENT PROTEINS (TIMI3, TIMI3, TIM44) (BY SI -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN: MITOCH INDER MEMBRANE (BY SIMILARITY). -1- SIMILARITY: BELONGS TO THE TIMI7/TIM22 FAMILY.		TIMITO. THATO. RATTUS NORVEGICUS (RAT). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.	1	SULT 1 17_RAT IMI7_RAT STANDARD; PRT; 171	ALIGNMENTS	44 69 7.6 406 1 TYRQ_HAEIN P44747 haemophilus 45 69 7.6 375 1 XYLH_HAEIN P45045 haemophilus
----------------------	--	--	---	---	--------	--	--	---	---	---	------------	--

STATE SOCIO CONTRACTO CONT

```
mitochondrial inner membrane protein involved in protein import."; FEBS LETT. 349:215-221(1994).
                                                                                                                                                                                                                                                                                                                               YEAST 12:787-797(1996)
                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
MEDLINE; 96408771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 75; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
59
88
113
33
                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGD; L0001139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123
                                                                                                                                                   import.
               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMIT_YEAST STANDARD; PRT; 158 AA.
P39515; 002310;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-UL-1998 (REL. 36, LAST ANNOTATION UPDATE)
MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM17
(MITOCHONDRIAL PROTEIN IMPORT PROTEIN 2) (MITOCHONDRIAL INNER MEMBRANE PROTEIN 2) (MITOCHONDRIAL INNER MEMBRANE PROTEIN MIM17).
                                                                                                                                                 BORBER U., RASSOW J., PPANNER N., MEIJER M., MAARSE A.C.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: COMPONENT OF THE PREPROTEIN IMPORT MACHINERY OF THE
MITOCHONDRIAL INNER MEMBRANE. INTEGRAL PART OF A PUTATIVE PROTEIN-
CONDUCTING CHANNEL OF THE MITOCHONDRIAL INNER MEMBRANE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 QIGGSFAVWGGLFXTIDCGLVRLRGKEDPWNSITSGALTGAVLAARSGPLAMVGSAMMGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MEEYAREPCPWRIVDDCGGAFTMGVIGGGVFQAIKGFRNAPVGIRHRLRGSANAVRIRAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM17 HOMOLOG.
                                                                                                                                                                                                                                                   SIMILARITY).
--- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AT LEAST 3 DIFFERENT PROTEINS (TIM7, TIM23, TIM44) (BY SIMILARITY)
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INDER MEMBRANE (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE TIM17/TIM22 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
STRAIN-ATCC 77162;
MEDLINE, 94326923.
MARREE A.C., BLOM J., KEIL P., PFANNER N., MEIJER M.;
"Identification of the essential yeast protein MIM17, an integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIMIT OR WILL OR MIMIT OR SMSI OR YJLI43W OR J0648.
SACCHAROWYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN TRANSPORT; TRANSMEMBRANE; MITOCHONDRION; INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILLALIEGVGILLTRYTAQQFRNAPPFLEDPSQLPPKDGTPAPGYPSYQQY 171
                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
77.2%; Score 703.5; DB .
Best Local Similarity 75.4%; Pred. No. 4.2e-57
Matches 129; Conservative 17; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6408C99C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18023 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X97544; E243529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 1
171 AA;
                                                                               (HUMAN)
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                   HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IM17_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
```

ŏ

g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 GGSFAVWGGLFXIIDCGLVRLRGKEDPWNSITSGALTGAVLAARSGPLAMVGSAMMGGIL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYAREPCFWRIVDDCGGAFTMGVIGGGVFQAIKGFRNAPVGIRHRLRGSANAVRIRAPQI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 DHSRDPCPIVILNDFGGAFAMGAIGGVVWHGIKGFRNSPLG--ERGSGAMSAIKARAPVL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The polytopic mitochondrial inner membrane proteins MIM17 and MIM23 "The polytopic mitochondrial inner membrane proteins MIM17 and MIM23 perate at the same preprotein import site."; FEBS LETT. 349:222-228(1994).
-!- FUNCTION: COMPONENT OF THE PREPROTEIN IMPORT MACHINERY OF THE MITOCHONDRIAL INNER MEMBRANE. INTEGRAL PART OF A PUTATIVE PROTEIN-CONDUCTING CHANNEL OF THE MITOCHONDRIAL INNER MEMBRANE.
-!- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AT LEAST 3 DIFFERENT PROTEINS (TIM17, TIM23, TIM44).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE.
MEDLINE; 95003211.
RYAN K.R., MENOLD M.M., GARRETT S., JENSEN R.E.;
"SMS1, a high-copy suppressor of the yeast mas6 mutant, encodes an
essential inner membrane protein required for mitochondrial protein
                                                                                                                                                                                                                                                                                                            KATSOULOU C., TZERMIA M., TAVERNARAKIS N., ALEXANDRAKI D.; "Sequence analysis of a 40.7 kb segment from the left arm of yeast chromosome X reveals 14 known genes and 13 new open reading frames including homologues of genes clustered on the right arm of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 94326924.
KUEBRICH M., KEIL P., RASSOW J., DEKKER P.J.T., BLOM J., MEIJER M.
PFANNER N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN TRANSPORT; TRANSMEMBRANE; MITOCHONDRION; INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.4%; Score 377.5; DB 1; Length 158; 48.7%; Pred. No. 1.3e-27; Live 26; Mismatches 50; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE TIM17/TIM22 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H -> T (IN REF. 2
8BDDCBFA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LALIEGVGILLTRYTAQQFR-NAPPFLEDPSQLP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                MOL. BIOL. CELL 5:529-538(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION, AND TOPOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X77796; G557267; -.
EMBL; S74018; G653752; -.
EMBL; X87311; G654554; -.
EMBL; 249418; G1015553; -.
SGD; L0001139; TIM17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
108
133
33
16584 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
```

; ;

AC DTT DTT DDT DDT DDT DTT DTT RX RX RX RX RX

122 LGVIEGVGLMFQRYAAWQAKPMAPPLPEAPSSQP 155

g

Wed Aug 11 10:51:20 1999

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŝ
                                                              15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM17 HOMOLOG
(MITOCHONDRIAL PROTEIN IMPORT PROTEIN 2) (MITOCHONDRIAL INNER MEMBRANE
                                                                                                                                                                                                                                                                                    BADCOCK K., CHURCHER C.M., WOOD V., BARRELL B.G., RAJANDREAM M.A.;
SUBMITIED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: COMPONENT OF THE PREPROTEIN IMPORT MACHINERY OF THE
MITOCHONDRIAL INNER MEMBRANE. INTEGRAL PART OF A PUTATIVE PROTEIN-
CONDUCTING CHANNEL OF THE MITOCHONDRIAL INNER MEMBRANE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 GGSFAVWGGLFXTIDCGLVRLRGKEDPWNSITSGALTGAVLAARSGPLAMVGSAMMGGIL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GGNFGVWGGLFSTFDCAVKGVRRKEDPWNAIIAGFFTGGALAVRGGWRATRNGAIGCACI 122
                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYAREPCPWRIVDDCGGAFTMGVIGGGVFQAIKGFRNAPVGIRHRLRGSANAVRIRAPQI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 DHTRDPCPYVILNDFGAAFSMGTIGGAIWHSIKGWRNSPPG-EKRISAIA-AAKTRAPVL 62
                                                                                                                                                                                                                                                                                                                                                                                              ΑT
                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AT LEAST 3 DIFFERENT PROTEINS (TIM17, TIM23, TIM44) (BY SIMILARITY -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN TRANSPORT; TRANSMEMBRANE; MITOCHONDRION; INNER MEMBRANE. TRANSMEM 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 LALIEGVGILLTRYTAQQFRNAPPFLEDPSQLPPKDGTPAPGYPS 167
                                                                                                                                                                                  EUKARYOTA; FUNCI; ASCOMYCOTA; ARCHIASCOMYCETES; SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.7%; Score 343.5; DB 1
43.6%; Pred. No. 1.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    044D336B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ā
                   164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REL. 36, CREATED)
(REL. 36, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                    SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                    36, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 E
16901 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z95395; E316107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89
114
164 AA;
                                                                                                                                                                                                                       SCHIZOSACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                   PROTEIN MIM17).
                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Simi
Matches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998
15-JUL-1998
                                               15-JUL-1998
                 IM17_SCHPO
P87130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IM22_SCHPO P87146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IM22_SCHPO
IM17_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DA PP
                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM22 HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 GG-----SFAVWGGLFXTIDCGLVRLRGKEDPWNSITSGALTGAVLAARSGPLAMVGS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 RIVDDCGGAFTM-GVIG---GGVFQAIKGFRNAPVGIRH-----RLRGSANAVRIRAPQI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DURSO G., LYE G., BOWMAN S., CHURCH C., WOOD V., BARRELL B.G.,
RAJANDREAM M.A., CONNOR R.E.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: ESSEWITAL COMPONENT OF MITOCHONDRIAL INNER MEMBRANE
PROTEIN IMPORT PATHWAY. INVOLVED IN THE IMPORT OF PROTEINS
TARGETED TO THE INNER MEMBRANE OF THE MITOCHONDRIAN SUCH AS
MITOCHONDRIAL CARRIER FAMILY MEMBERS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAHR A., MOELLER-RIEKER S., HANKELN T., KRAEMER C., SCHMIDT E.R.; SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIM22 OR YDL217C OR D0884.
SACCHAROWYCES CERVISIAE (BAKER'S YEAST).
EUKARYOTA, FUNGI, ASCOMYCOTA, HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSPORT; TRANSMEMBRANE; MITOCHONDRION; INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Indels
                                               SCHIZOSACCHAROMYCES POMBE (FISSION YEAST),
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 117; DB 1;
Pred. No. 0.00053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
BE82B517 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 AMMGGILLALIEGVGILLTRYTAQOF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 PC
18641 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.8%;
26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 295397; E315883; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S288C / FY1679;
                                                                                                     SCHIZOSACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IM22_YEAST
012328:
                                                                                                                                                     STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

. 9

```
131
145
167
175
190
197
222 AA;
                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its Modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1993 (REL. 27, CREATED)
01-0CT-1993 (REL. 27, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 37, LAST ANNOTATION UPDATE)
MITOCHONDRIAL IMPORT NINER MEMBRANE TRANSLOCASE SUBUNIT TIM23
(MITOCHONDRIAL PROTEIN IMPORT PROTEIN 3) (MITOCHONDRIAL PROTEIN IMPORT PROTEIN MACHINERY PROTEIN MIM23).
TIM23 OR MASG OR MPI3 OR MIM23 OR VINGITWOR N3180.
SACCHAROMYCES CEREVISIAE (BAKER'S SIBARIAL CARACHAROMYCES CEREVISIAE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 TAGNIGVGGISKIVQQISDLP--FRQQMKLQFTDMGKKSYSSAKNFGYIGMIYAGVECVI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 TMGVIG-GGVFQAIKGFRNAPVGIRHRLRGSANAVRIRAPQIGGSFAVWGGLFXTIDCGL 80
                                                                                          SEQUENCE FROM N.A.
MEDLINE; 93359499.
EMTAGE J.L.T., JENSEN R.E.;
"MANG encodes an essential inner membrane component of the yeast
mitochondrial protein import pathway.";
J. CELL BIOL. 122:1003-1012(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES
                                                               SIRRENBERG C., BAUER M.D., GUIARD B., NEUPERT W., BRUNNER M.; "Import of carrier proteins into the mitochondrial inner membrane mediated by Tim22.":
                                                                                                                                                                                                                                                                                                                   EMBL; X99000; E253394; -.
EMBL; Z74265; E253267; -.
SGD; L0004157; TIM22.
PROTEIN TRANSPORT; TRANSMEMBRANE; MITOCHONDRION; INNER MEMBRANE.
TRANSMEM 47 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.7%; Score 115.5; DB 1; Length 207; 30.0%; Pred. No. 0.00086; tive 23; Mismatches 40; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 93380573.
DEKKER P.J.T., KEIL P., RASSOW J., MAARSE A.C., PFANNER N.,
         RASMUSSEN S.W.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE TIM17/TIM22 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 VRLRGKEDPWNSITSGALTGAVLAARSGPLAMVGSAMMGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
AA8B8201 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 AA.
                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                     207 AA; 21864 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0uery Match
Best Local Similarity 30.03
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                       INNER MEMBRANE.
                                                             97113414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IM23_YEAST
P32897;
                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEAST
```

g ö

ò

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 GAVYLLGLGIGGFSGMMQGLQNIPPNSPGKLQLNTVLNHITKRGPFLGNNAGILALSYNI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 GGAFTMGVIGGGVFQAIKGFRNAPVGIRHRLRGSA--NAVRIRAPQIGGSFAVWGGLFXT 75
                                                                                                                                                                                                                                                     MEIJER M ;
"Identification of MIM23, a putative component of the protein import
"Identification of the mitochondrial inner membrane.";
FEBS LETT. 330:66-70(1993).
                                                                                                                                                                                                MEDLINE; 94326924.
KUEBRICH M., KEIL P., RASSOW J., DEKKER P.J.T., BLOM J., MEIJER M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD; L0001028; WAS6.
MITOCHONDRION; INNER MEMBRANE; TRANSPORT; PROTEIN TRANSPORT;
TRANSMEMBRANE; TRANSLOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 104; DB 1; Length 222;
Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 IDCGLVRLRGKEDPWNSITSGALTGAVLAARSG--PL----AMVGSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERMEMBRANE (POTENTIAL).
320C2078 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERMEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERMEMBRANE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
MATRIX (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.4%; Score 104; DB
Best Local Similarity 29.9%; Pred. No. 0.01
Matches 32; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE TIM23 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 PO
196 MA
215 PO
222 IN
23243 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUTM_NEUCR

NUTM_NEUCR STANDARD;

AC P25710;

DT 01-MAY-1992 (REL. 22, CREATED)
                                                                                                                                                                                    CHARACTERIZATION, AND TOPOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X71633; G297118; --
EMBL; X74161; G402785; --
EMBL; Z71632; E299788; --
PIR; S33201; S33201.
PIR; S36139; S36139.
PIR; A40705; A40705.
```

'n

SO WENT TO THE SOURCE OF THE PROPERTY OF THE P

```
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNTHESIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYASE; CAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPYR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
KPYR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DT DT DT DT OS OS
       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and its an analysis and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÷
                                                                                                                                                                                                                                                       NADH:ubiquinone reductase (complex I) from Neurospora crassa.";
BIOCHIM. BIOCHIYS. ACTA 1088:325-326(1991).
-!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
TO BE UBIQUINONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GG---SFAVWGGLFXTIDCGLVRLRGKEDPWNSITSGALTGAVLAARS--GPLAMVGSAM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 GGTIISFTLAGGIYRFAQQASANLREKEDGWNHAIGAFLGGSVMGLRSLRFPVILGFGAM 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 MGGILLALIEGVGIL------LTRYTAQQFRNAPPFLEDPSQLPPKDGTPAPGY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: NADH + UBLQUINONE = NAD(+) + UBLQUINOL. SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS. SUBCELLULAR LOCATION: MATRIX AND CYTOPLASMIC SIDE OF THE MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1993 (REL. 27, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE)
(ADENYLAT CYCLASE).
                                                                                                                                                                                                                                        'CDNA and genomic DNA sequence of the 21.3 kDa subunit of NADH:ubiquinone reductase (complex I) from Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                NEHLS U., HEMMER S., ROEHLEN D.A., VAN DER PAS J.C., PREIS D.,
SACKMANN U., WEISS H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 200;
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE 21.3 KD SUBUNIT (EC 1.6.5.3)
                                                                       NEUROSPORA CRASSA.
EUKARYOTA: FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER, KIDNEY, AND HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.8%; Score 89.5; DB 1; Best Local Similarity 27.1%; Pred. No. 0.19; Matches 32; Conservative 14; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21349 MW; A0B12273 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ST. LAWRENCE 74 / SL 74 / ORS 6A;
                                                                                                           SORDARIALES; SORDARIACEAE; NEUROSPORA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 164-1262 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RATTUS NORVEGICUS (RAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X56612; G3050; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 AA;
                                                                                                                                                                               MEDLINE; 91159490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=LIVER;
MEDLINE; 93028552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PREMONT R.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYA5_RAT
Q04400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
```

g

ò

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 WRGGDDDEDPPLSGDDPLVGGFGF----SFRSKSAWQERGGDDGGRGSRRQRRGAAGGGS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 TRAPPAGGSGSSAAAAAAGGTEVRPRSVEVGLEERRGKGRAAEELEPGTGTVEDGDGSE 188
                                                             adenylyl cyclases.";
PROC. NATL. ACAD. SCI. U.S.A. 89:9809-9813(1992).
-!- FUNCTION: THIS A MEMBRANE-BOUND, CALMODULIN-INSENSITIVE ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 WRIVDDCGGAFTMG---VIGGGVFQAIKGFRNAPV------GIRHRLRGSANAVR 56
                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
-:- ENZYME REGULATION: INSENSIBLE TO CA(2+)/CALMODULIN. STIMULATED
THE G PROTEIN BETA & GAMMA SUBUNIT COMPLEX.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS TWO
DOMAINS WITH 6 POTENTIAL TRANSMEMBRANE REGIONS EACH.
-!- SIMILARITY: THE TWO CYTOPLASMIC DOMAINS ARE SIMILAR TO ONE
ANOTHER AND TO THE CATALYTIC DOMAINS OF GUANYLATE CYCLASES.
PREMONT R.T., CHEN J., MA H.-W., PONNAPALLI M., IYENGAR R.; "TWO members of a widely expressed subfamily of hormone-stimulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEMBRANE; GLYCOPROTEIN; DUPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.4%; Score 86; DB 1; Length 1262; 26.2%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 IRAPQIGGS-----FAVWGGLF---XTIDCGLVRLRGK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL). POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LGACCLALLQ 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 DPWNSITSGALTGAVLAARSGPLAMVGSAMMGGILLALIE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3F17897B CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P30613; P11973;
01-ARR-1993 (REL. 25, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PYRUVATE KINASE, ISOZYMES R/L (EC 2.7.1.40).
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              574 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00452; GUANYLATE_CYCLASES; 2. PFAM; PF00211; guanylate_cyc; 2. HSSP; P19754; lAWK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 DGGSSVASGSGTGTVLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1262 AA; 139178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 26.2%;
Matches 42; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M96159; G1758332; -.
```

7;

```
MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM;
                                                                                                                                                                                                                                                                                                                        (HNHA)
MEDLINE; 93244440.

KANNO H., FUJII H., MIWA S.;

"Low substrate affinity of pyruvate kinase variant (PK Sapporo)
caused by a single amino acid substitution (426 Arg-->Gln) associated
with hereditary hemolytic anemia.";

BLOOD 81:2439-2441(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [10]
VARIANIS S-332; S-336; K-354 DEL; D-361; T-392; H-498; Q-510 & W-532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Point mutations in the L-type pyruvate kinase gene of two children with hemolytic anemia caused by pyruvate kinase deficiency."; BLOOD 77:1871-1875(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAND H., FUJII H., HIRONO A., OMINE M., MIWA S.; TANNO H., FUJII H., HIRONO A., OMINE M., MIWA S.; Talentical point mutations of the R-type pyruvate kinase (PK) cDNA found in unrelated PK variants associated with hereditary hemolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KANNO H., FUJII H., TSUJINO G., MIWA S.;
KANNO H., FUJII H., TSUJINO G., MIWA S.;
"Molecular basis of impaired pyruvate kinase isozyme conversion in erythroid cells: a single amino acid substitution near the active site and decreased mRNA content of the R-type PK.";
BIOCHEM. BIOPHYS. RES. COMMUN. 192:46-52(1993).
                                                                                                              of
                                                                                                                                                                                                                                                       TANI K., FUJII H., NAGATA S., MIWA S.;
"Human liver type pyruvate kinase: complete amino acid sequence and the expression in mammalian cells.";
PROC. NATL. ACAD. SCI. U.S.A. 85:1792-1795(1988).
                                                                                       KANNO H., FUJII H., HIRONO A., MIWA S., FARANO H., FUJII H., HIRONO A., MIWA S., CDNA Cloning of human R-type pyruvate kinase and identification single amino acid substitution (Thr384-->Met) affecting enzymatic stability in a pyruvate kinase variant (PK Tokyo) associated with hereditary hemolytic anemia.";
PROC. NATL. ACAD. SCI. U.S.A. 88:8218-8221(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BARONCIANI L., BUTLER E.; "Ahalysis of pyruvate kinase-deficiency mutations that produce nonspherocytic hemolytic anemia.";
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 87184521.
TANI K., FUJI H., TSUTSUMI H., SUKEGAWA J., TOYOSHIMA K.,
YOSHIDA M.C., NOGUCHI T., TANAKA T., MIWA S.;
"Human liver type pyruvate kinase: cDNA cloning and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 91208396.
NEUBAUER B., LAKOMEK M., WINKLER H., PARKE M., HOFFERBERT S.,
SCHROTER W.;
     VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS D-134; P-155; H-359; W-486; V-495 AND Q-510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROC. NATL. ACAD. SCI. U.S.A. 90:4324-4327(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 365-431 FROM N.A., AND VARIANT OSAKA.
MEDLINE; 93236593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   assignment.";
BIOCHEM. BIOPHYS. RES. COMMUN. 143:431-438(1987).
                                                            SEQUENCE FROM N.A., AND VARIANT TOKYO. MEDLINE; 91376115.
                        PRIMATES; CATARRHINI; HOMINIDAE; HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 96263732.
BEUTLER E., BARONCIANI L.;
"Mutations in pyruvate kinase.";
HUM. MUTAT. 7:1-6(1995).
             CHORDATA;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 470-574 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT FUKUSHIMA/MAEBASHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS SAPPORO GLN-426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOOD 79:1347-1350(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS LINZ AND BEIRUT.
MEDLINE; 91208396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVIEW ON VARIANTS.
MEDLINE; 96263732.
             EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93248282
                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 88158079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 92163106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anemia
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ц
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYCOLYTIC ENZYMES.

THERE ARE 4 ISOZYMES OF PYRUVATE KINASE IN MAWMALS: L, R, MI AND THERE ARE 4 ISOZYMES OF PYRUVATE KINASE IN AIS FOUND IN RED M2. L TYPE IS MAJOR ISOZYME IN THE LIYER, R IS FOUND IN AND M2 IS FOUND IN EARLY FETAL TISSUES.

ALTERNATIVE PRODUCTS: THE L- AND R-TYPE ISOZYMES ARE PRODUCED FROM A SINGLE GENE BY USE O DIFFERENT PROMOTERS. THE SEQUENCE SHOWN HERE IS THAT OF THE R-TYPE.

SHOWN HERE IS THAT OF THE R-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFERASE; KINASE; GLYCOLYSIS; MULTIGENE FAMILY; PHOSPHORYLATION;
MAGNESIUM; ALTERNATIVE SPLICING; DISEASE MUTATION.
    EBRANER C., NUERNBERG P., THIELE B.-J., REIS A., BRABEC V.,
SARALOVA A., JACOBASCH G.;
"Mutations in the pyruvate kinase L gene in patients with hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 98141680.

PASTORE L., DELLA MRTE R., FRISSO G., ALFINITO F., VITALE D., PASTORE L., DELLA MRRER F., ZAGARI A., ROTOLI B., SALVATORE F.;

"Novel mutations and structural implications in R-type pyruvate kinase-deficient patients from Southern Italy.";

HUM, WUTAT, 11:127-134(1998).

-1- CATALYTIC ACTIVITY: ATP + PRRUVATE = ADP + PHOSPHOENOLPYRUVATE.

-1- COPACTOR: REQUIRES MAGNESIUM AND POTASSIUM.

-1- PATHMXY: FINAL STEP IN GIXCOLYSIS.

-1- SUBMITH HOMOTETRAMER.

-1- SUBMITH HOMOTETRAMER.

-1- DISEASE: DEFECTS IN PYRUVATE KINASE ARE THE MOST COMMON CAUSES FOR HEREDITARY NONSPHEROCYTIC HEMOLYTIC ANEMIA (HNSHA) AMONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 99043610.

ZARZA R., ALVAREZ R., PUJADES A., NOMDEDEU B., CARRERA A., ESTELLA REMACHA A., SANCHEZ J.M., MOREY M., CORTES T., PEREZ LUNGMUS G., NOMDEOLU B., PEREZ LUNGMUS G., NOMERO B., VIVES CORRONS J.L.;

"Molecular characterization of the PK-LR gene in pyruvate kinase deficient Spanish patients.";

BR. J. HAEMATOL. 103:377-382(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BARONCIANI L., WESTWOOD B., BEUTLER E.; "Study of the molecular defects in pyruvate kinase (PK) deficient patients affected by hereditary nonspherocytic hemolytic anemia
                                                                                                                                                                                                                                                                                                     PARONCIALY L., BEUTLER E.; Molecular study of pyruvate kinase deficient patients with molecular study of pyruvate hereditary nonspherocytic hemolytic anemia."; J. CLIN. INVEST. 95:1702-1709(1995).
                                                                                                                                                                                                                           VARIANTS E-331; A-341; K-393; S-393; D-458; M-460 AND H-498
REIS A., BRABEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS HNSHA S-332; P-337; W-486; C-498 AND Q-510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00110; PYRUVATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INVEST. MED. 43:341A-341A(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D10326; G220036; --
EMBL; M15465; G189996; --
ERRE, S60712, G299641; --
PIR; A30150; A30150.
PIR; A29414; A29414.
SWISS-ZDPAGE; P30613; HUMAN.
MIM; Z66200; --
PROSITE; PS00110; PYRUVATE_KIP
                                                                                                                                                             BLOOD 83:2817-2822(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00224; PK; 1.
P11974; 1PKN.
                                                                                                                                                                                                                                                                                 95221622
                                                                                                                                hemolytic anemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS HNSHA
```

AND ALTERNATIVE SPLICING

```
ñ
                                                                                                          MISSING (IN HEMOLYTIC ANEMIA).

MISSING (IN HEMOLYTIC ANEMIA).

V -> D (IN HEMOLYTIC ANEMIA).

V -> D (IN HEMOLYTIC ANEMIA).

E -> Q (IN HEMOLYTIC ANEMIA).

E -> Q (IN HEMOLYTIC ANEMIA).

E -> Q (IN HEMOLYTIC ANEMIA).

D -> D (IN HEMOLYTIC ANEMIA).

G -> R (IN HEMOLYTIC ANEMIA).

D -> D (IN HEMOLYTIC ANEMIA).

I -> T (IN HEMOLYTIC ANEMIA).

R -> S (IN HEMOLYTIC ANEMIA).

R -> S (IN HEMOLYTIC ANEMIA).

R -> D (IN HEMOLYTIC ANEMIA).

I -> T (IN HEMOLYTIC ANEMIA).

MISSING (IN HEMOLYTIC ANEMIA).

R -> C (IN HEMOLYTIC ANEMIA).

R -> C (IN HEMOLYTIC ANEMIA).

N -> D (IN HEMOLYTIC ANEMIA).

D (IN HEMOLYTIC ANEMIA).

N -> D (IN HEMOLYTIC ANEMIA).

D (IN HEMOLYTIC ANEMIA).

N -> D (IN HEMOLYTIC ANEMIA).

N -> D (IN HEMOLYTIC ANEMIA).

N -> D (IN HEMOLYTIC ANEMIA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.

MAGNESIUM (POTENTIAL).

MAGNESIUM (POTENTIAL).

MAGNESIUM (POTENTIAL).

MAGNESIUM (POTENTIAL).

MSIQENISSLQLRSWVSKSQRDLAKSILIGAPG -> ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A -> T (IN HEMOLYTIC ANEMIA).
n -> K (IN HEMOLYTIC ANEMIA).
n -> S (IN HEMOLYTIC ANEMIA).
c -> CS (IN HEMOLYTIC ANEMIA).
T -> I (IN HEMOLYTIC ANEMIA).
0 -> K (IN HEMOLYTIC ANEMIA).
AREBASHI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MEEYAREPCPWRIV----DDCGGAFTMGVIGGGVFQAIKGFRNAPVGI----RHRLRGSA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> Q (IN HEMOLYTIC ANEMIA; SAPPORO)
-> W (IN HEMOLYTIC ANEMIA).
-> T (IN HEMOLYTIC ANEMIA).
-> D (IN HEMOLYTIC ANEMIA).
-> V (IN HEMOLYTIC ANEMIA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 NAVRIRAPQIGGSFAVWGGLFXTIDCGLVRLRGKEDPWNSITSGALTGAVLAARSG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 574;
     PHOSPHORYLATION (BY CAPK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 2.2;
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 26.7% nes 31; Conservative
   43
313
315
336
337
33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392
393
393
401
408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426
426
431
458
459
MOD_RES
ACT_SITE
METAL
                                                                   METAL
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match
                                                                                                                                                                                                    VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                     VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                     VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                    VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
VARIANT
                                                                                                                   VARIANT
                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                    VARIANT
                                                                                                                                                     VARIANT
                                                                                                                                                                   /ARIANT
                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ĘΣ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   بب
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 CGLVRLRGKEDPWNSITSGALTGAVLAARS-GPLAMVGSAMMGGILLALIE-GVGILLTR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 CGVLWLSGHGHSWLQNTTDLISSSLTVLNHLGPVAWLGSGTWGIPSLLLVSLTVSLVIVT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISSING (IN STEP20 AND STEP46).
GYSGEEKVYI -> VCSSIPRAFH (IN STEP38 AND
                                                                                                                                                                                                                                   Ø
                                                                                                                                                                  SHARMA E., ZHAOFF., BULT A., LOMBROSO P.J.;
SHARMA E., ZHAOFF., BULT A., LOMBROSO P.J.;
Ildentification of two alternatively spliced transcripts of STEP:
subfamily of brain-enriched protein tyrosine phosphatases.";
BRAIN RES. MOL. BRAIN RES. 32:87-93(1995).
-!- CATALVITIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
PROTEIN TYROSINE + ORTHOPHOSPHATE.
-!- TISSUE SPECIFICITY: STEP2O IS EXPRESSED ONLY IN THE CNS.
-!- TISSUE SPECIFICITY: STEP2O IS EXPRESSED ONLY IN THE CNS.
-!- ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS ARE PRODUCED BY
ALTERNATIVE PRICING: STEP2O LACK THE CATALVITIC DOMAIN.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
SERINE HYDROXYMETHYLLTRANSFERASE (EC 2.1.2.1) (SERINE METHYLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STEP20).
MISSING (IN STEP38 AND STEP20).
9C9F4460 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.1%; Score 83; DB 1; Length 541; 28.9%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACTERIA; SPIROCHAETALES; SPIROCHAETACEAE; BORRELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPIROCHETE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Shail).
GLYA OR BB0601.
BORRELIA BURGDORFERI (LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 YTAQQFRNAPPFLEDPSQLPPKD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYROSINE PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00102; Y_phosphatase; 1.
HSSP; P18052; 1YFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYDROLASE; ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQI
15-DEC-1998 (REL. 37, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 M
60829 MW;
[1]
SEQUENCE FROM N.A., AND ALTER
STRAIN=BALB/C; TISSUE=BRAIN;
MEDLINE; 96115113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S80329; G1245880; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U28217; G915382; -. EMBL; U28216; G915380; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.1
Best Local Similarity 28.9
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:97807; PTPNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 35210 /
MEDLINE; 98065943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYA_BORBU
O51547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
GLYA_BORBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SHMT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID DATE OF THE STATE OF THE STA
    STATE THE TANK AND DESCRIPTION OF THE THE TANK AND DESCRIPTION OF THE THE TANK AND DESCRIPTION OF THE THE TANK AND DESCRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

us-09-208-619-1.rsp

```
DC11_DROME
P18169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     events."
                                                                                                       TRANSMEM
                                                                                                                            SEQUENCE
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration,
                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>.</u>
PRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M.,
DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.,
VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WELDMAN J.,
UTTERBACK T., WAITHEY L., WCDONALD L., ARTIACH P., BOWMAN C.,
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
SMITH H.O., VENIER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 AVWGGLFXTIDCGLVRLRGKEDP-WNSITSGALTGAVLAARSGPLAMVGSAMMGGILLAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 ILSGRDFDK----LVNFNGKEKPLFNAVNSTVFPG----TQGGPLVHV----IAGKAIAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-H37RV;
CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.,
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 IVDD-----CGGAFTMGVIGGGVFQAIKGFRNAPVGIRHRLRGSANAVRIRAPQIGGSF 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE; MYCOBACTERIUM ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                           TRANSFERASE; PYRIDOXAL PHOSPHATE: ONE-CARBON METABOLISM.
221 221 221 SPRIDOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 417 AA; 45881 MW; D070203A CRC32;
                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 417;
                                                                                             Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (REL. 34, CREATED).
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 27.8 KD PROTEIN CY251.08.
                                                                                                                                                                                                                                                                                                                                                                                                                                      8.8%; Score 80.5; Di
26.4%; Pred. No. 2.6;
cive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 IEGVGILLTRYTAQQFRNAPPFLE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 KEALQESFKEYIANVIKNTKVMAE 302
                                                                                                                                                                                                                                                                                                                                              EMBL; AE001161; G2688518; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYCOBACTERIUM TUBERCULOSIS.
                                                                                                                                                                                                                                                                                                                                                                    PS00096; SHMT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y058_MYCTU
Q10887;
                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
Y058_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STEETHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
   between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
matics and the EMBL outstation
There are no restrictions on it
gg as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 ----GSFAVW-----GGLFXTIDCGLVRLRGKEDPWNSITSGALTGAVLAARSGPLAM 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEV. 142:1-12(1990).

-1 FUNCTION: THE DEC-1 FEMALE-STERILE LOCUS PROTEIN IS REQUIRED
-1 FUNCTION: THE DEC-1 FEMALE-STERILE SEGSHELL.
FOR PROPER ASSEMBLY OF THIP DE PROTEINS ARE PRODUCED FROM THE
-1 FALTERNATIVE PRODUCTS: WULTIPLE PROTEINS ARE PRODUCTIC CLEAVAGE
DEC-1 GENE BY ALTERNATIVE RNA SPLICING AND PROTEOLYTIC CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 WRIVDDCGGAFTMGVIGGGVFQAIKGFRNAPVGIRHRLRGSA--NAVRIRAPQIG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WRCL-RCGD-FALGGPQG-----RGAPEDAPLIMRGKALRQAIIIRALGVERLVRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 91033553.
WARING G.L., HAWLEY R.J., SCHOENFELD T.;
"Multiple proteins are produced from the dec-1 eggshell gene in ranitiple proteins are produced from the dec-1 brosophila by alternative RNA splicing and proteolytic cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFECTIVE CHORION-1 FC125 PROTEIN.
12 X 26 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA, METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA, DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLYBASE; FBGN0000427; dec-1.
CHORION; EGGSHELL; REPEAT; ALTERNATIVE SPLICING; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DEFECTIVE CHORION-1 FC125 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                5EDAB7C2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.8%; Score 80.5; Di
26.2%; Pred. No. 1.6;
Live 20; Mismatches
                                                                                                                                                                                                                                                                     HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
TRANSMEM 155 175 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 VGSAMMGGILLALIEGVGILLTRYTAQQF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                27837 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M35887; G157182; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DROSOPHILIDAE; DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                              EMBL; 274410; E249404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A44766; A44766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 91032553.
                                                                                                                                                                                                                                                                                                                                                                          256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 39; Conserv
```

SEQUENCE

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-ATCC 13869;
YOON K.H.;
SUBMITTED (NOV-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLEVER ACTIVE
-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLEVER ACTIVE
--- THE SUGAR BINDING SITE
---- THE DOMAIN CONTAIN THE SUGAR BINDING SITE
---- THA DOMAIN CONTAINS THE PRIMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDBATE ACTIVE—TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO THE SUGAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                            1010 FTYGEGLLHPF-MGLLPVERPDDFWNQKPYDPHHPLYTGGGSYDAYL--RDGRHRRDTHI 1066
                                                                                                                                                                                                                                                                                                        952 GEVGGSESO--KSNSNPPTTLTPAPQEQPQEHRVHKSPSSAPSETEIENAPSSDPQVGSI 1009
                                                                                                                                                                                                                                                                                                                                                                           66 FAVWGGLEXTIDCGLVRLRGKEDPWNS-----ITSGALTGAVLAARSG----PLAM 112
                                                                                                                                                                           52; Gaps
                                                                                                                                                                                                                                       24 GVIGGGVFQAIKGFRNAPVGI------RHRLRGSANAVRIRA------PQIGGS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 VGSAMMGGILLALIEGVGIL--LTRYTAQQFRNAPPFLEDPSQLPPKDGTPAPGYPSY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLUCOSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PLS SYSTEM, GLUCOSE-SPECIFIC IIABC COMPONENT (EIIABC-GLC) (G)
PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC
COMPONENT) (EC 2.7.1.69) (EII-GLC / EIII-GLC).
                                                                                            8.8%; Score 80; DB 1; Length 1123; 24.7%; Pred. No. 8.3; ive 16; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHOTRANSFERASE SYSTEM; SUGAR TRANSPORT; TRANSFERASE; PHOSPHORYLATION; TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BREVIBACTERIUM LACTOFERMENTUM.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; CORYNEBACTERIACEAE;
CORYNEBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
-:- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EILE DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EILE DOMAIN.
99218239 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  674 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN.
DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIIB EIIC EEIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00371; PTS_EIIA_1; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
PFAM: PF00358; PTS_EIIA_1; 1.
PFAM: PF00367; PTS_EIIB, 1.
HSSP; P08837; 2F3G.
127959 MW;
                                                                                                                                                                       44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L18875; G405143; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
1123 AA;
                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTGA_BRELA
                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  045298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRELA
                                                                                                                                                                    Matches
So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A THE TARKET AND DESCRIPTION OF THE 
                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
```

```
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 QIGGSFAVWGGLFXTIDCGLVRLRGKEDPWNSITSGALTGAVLAARSGPLAMVGSAMMGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| | :| | :| | :| 335 TLGYDF-------IQGPMGAWNFACFGLVTGVFLIALKEKNRAMRQVSLGG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 GPFGIGV-GNGISSLLEAVNNFSPFILSIVIPLLYPFLVPLGLHWPL----NAIMIQNLN 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- APVGIRHRLRGSANAVRIR-AP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
C21F0F14 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 6;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ILLALIEGV-----GILLTRYTAQQFRNAP 145
                                                                                            POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 79;
                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 MLAGLLGGISEPSLYGVLL-RFKKTYFRLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                              71626 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 GAFTMGVIGGGVFQAIKGFRN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  674 AA;
11126
3322233222333260
334444
524444
5233360
5233
                                                                                                                                                                                                TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
TRANSMEM
                                                                                                   FRANSMEM
                                                                                                                            TRANSMEM
                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                       TRANSMEM
                                FRANSMEN
                                                                       TRANSMEN
                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                              RES
                                                                                                                                                                                                                                                                                                                                                                           MOD
SETT LE FET LE SET LE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

Search completed: August 10, 1999, 08:35:42 Job time: 8499 sec

THIS PAGE BLANK (USPTO)

SSI dossawa ייי גייי ביי ביי אר

APPLICANT: Kuhatoss, Stuart A., Ar. Rosteck, Paul R., Jr. Applicant: Sutton, Kimberly L.
TILLE OF INVENTION: POLYKETIDE SYNTHASE GENES

DeHoff, Bradley S

Sequence 11, Application US/08804227C Patent No. 5876991

9

and the Market of the second

9

APPLICANT:

N2-08-804-333C-11

THIS PAGE BLANK (USPTO)

```
Appl
Appl
Appl
Appl
Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appli
Appli
                                                                                                                                                                                                                                                                                                                  Sequence 11, Appl
Sequence 12, Appl
                                              August 10, 1999, 06:10:21 ; Search time 9.9 Seconds (without alignments) 171.451 Million cell updates/sec
                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                    Sequence 8, A Sequence 40, Sequence 18,
                                                                                                                                                                                                                                                                                                                                                            Sequence 17,
Sequence 17,
Sequence 15,
Sequence 25,
Sequence 25,
Sequence 29,
Sequence 29,
                                                                                   US-09-208-619-1
911
1 MEEYAREPCPWRIVDDCGGA.....QLPPKDGTPAPGYPSYQQYH 172
                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                 /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/FB_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS9_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pacKfiles1.pep:*
         Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                   US-08-638-911A-25
US-08-638-911A-25
US-08-638-911A-27
US-08-638-911A-27
US-08-638-911A-37
US-08-444-73-15
US-08-444-73-15
US-08-464-134-15
US-08-465-910-15
US-08-465-910-15
US-08-465-910-183
US-08-461-34-183
US-08-461-361-183
US-08-485-618-4
US-08-173-497-4
                                                                                                                                                                                                                                                                                                        US-08-812-645-4
US-08-804-227C-11
US-08-804-227C-12
US-08-673-789-8
US-08-673-739A-40
                                                                                                                                                                                                                                                                                                                                                    PCT-US95-04681-18
                                                                                                                                                                                                                                                                                                                                                            US-08-804-227C-4
US-08-216-276A-17
US-08-466-033-15
GenCore version 4.5
Copyright (c) 1993 - 1998 Com
                                                                                                                                       106577 seqs, 9868381 residues
                                                                                                                                                                                                                                              SUMMARIES
                                  OM protein - protein search, using sw model
                                                                                                                                                        Issued_Patents_AA:*
                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                          BLOSUM62
                                                                                                                                                                                                                                                               Query
                                                                                                                                                                                                                                                                                               703.5
377.5
78
74
                                                                                                                                                                                                                                                                                                                                  72.5
72.5
72.5
71.5
                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                       606
                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                        se:
                                                                                                                                       Searched:
                                                                                                      Sequence:
                                                  Run on:
                                                                                                                                                                                                                                                              Result
No.
```

Sequence 19, Sequence 8, A Sequence 44, Sequence 44,

US-08-370-909-19 US-08-504-048-8 US-08-476-062A-44 PCT-US96-01314-44

Sequence

Sequence

Sequence Sequence

```
ö
    Appl
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
   Sequence 42,
Sequence 43,
Sequence 3, A
Sequence 5, A
Sequence 5, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEEYAREPCPWRIVDDCGGAFTMGVIGGGVFQAIKGFRNAPVGIRHRLRGSANAVRIRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIGGSFAVWGGLFXTIDCGLVRLRGKEDPWNSITSGALTGAVLAARSGPLAMVGSAMMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ILLALIEGVGILLTRYTAQQFRNAPPFLEDPSQLPPKDGTPAPGYPSYQQYH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.8%; Score 909; DB 2; I
100.0%; Pred. No. 1.1e-97;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: GOLI, SURYA K.
TITLE OF INVENTION: NOVEL HUMAN MITOCHONDRIAL
TITLE OF INVENTION: MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
US-08-467-822-42
US-08-467-822-43
US-07-985-458-3
US-08-462-884A-3
US-07-891-942G-5
US-08-461-881B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,645
                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: TO BE Assigned FILING DATE: Filed Herewith ATTORNEY/ACENT INFORMATION:
NAME: Billings, Lucy J. RESISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0229 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \mathbf{u}
                                                                                                                                                                                                      Sequence 1, Application US/08812645
Patent No. 5854414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 172; Conservative
 196
199
738
605
560
605
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein IMMEDIATE SOURCE: LIBRARY: BLADNOT04 CLONE: 1318463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ropology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-812-645-1
                                                                                                                                                                         RESULT 1
US-08-812-645-1
 65
64 . 5
64 . 5
64 . 5
64 . 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
```

셤

```
63 GGSFAVWGGLFXTIDCGLVRLRGKEDPWNSITSGALTGAVLAARSGPLAMVGSAMMGGIL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 GGNFGVWGGLFSTFDCAVKAVRKREDPWNAIIAGFFTGGALAVRGGWRHTRNSSITCACL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 EYAREPCPWRIVDDCGGAFTMGVIGGGVFQAIKGFRNAPVGIRHRLRGSANAVRIRAPQI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.4%; Score 377.5; DB 2;
48.7%; Pred. No. 2.4e-36;
tive 26; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DeHoff, Bradley S.
APPLICANT: Ruhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MITOCHONDRIAL
TITLE OF INVENTION: MEMBRANE PROTEIN
NUMBER OF INVENTIOS: 4
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          SOFTWARE: FASTSED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,645
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 LALIEGVGILLTRYTAQQFR-NAPPFLEDPSQLP 155
                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: TO BE Assigned
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0229 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 11, Application US/08804227C; Patent No. 5876991
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 158 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 41.4%
Best Local Similarity 48.7%
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIAL.
LIBRARY: General - ANTE: GI 557267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE
                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
  Patent No. 5854414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11:
                                                                                                                                                                                                                                            COUNTRY: UX
ZIP: 94304
                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-08-804-227C-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CLONE: C
US-08-812-645-4
                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MEEYAREPCPWRIVDDCGGAFTMGVIGGGVFQAIKGFRNAPVGIRHRLRGSANAVRIRAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MEEYAREPCPWRIVDDCGGAFTMGTIGGGIFQAIKGFRNSPVGVNHRLRGSLTAIKTRAP 60
121 ILLALIEGVGILLTRYTAQQFRNAPPFLEDPSQLPPKDGTPAPGYPSYQYH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ILLALIEGVGILLTRYTAQQFRNAPPFLEDPSQLPPKDGTPAPGYPSYQQY 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.2%; Score 703.5; DB 2 Best Local Similarity 75.4%; Pred. No. 6.1e-74; Matches 129; Conservative 17; Mismatches 24
                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MITOCHONDRIAL
TITLE OF INVENTION: MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,645
                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-0229 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO Be Assigned
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-08-812-645-4
; Sequence 4, Application US/08812645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
TELEDOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                  Sequence 3, Application US/08812645
Patent No. 5854414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 171 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: GenBank
CLONE: GI 1770564
                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: G
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                              RESULT 2
US-08-812-645-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH:
                                                                                                                                                                                                                                                                                                                                                                 STATE:
```

5;

Op

ò

δ

유

g

ò

```
1239 VTGGL-GGVGGHVARWLARSGAEHVVLAGRRGGGVVGAVELERELVGLGAKVTFVSCDVG 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VWGGLFXTIDCGLVRLRGKEDPWNSITSGALTGAVLAARSGPLAMVG------ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 WRIVDDC---GGAFTMGVIGGGVFQAIKGFRNAPVGIRHRLRGSANAVRIRAPQIGGSFA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ZHOW, RENPING; SCHULZ, NICHOLAS,
APPLICANT: ZHOW, RENPING; SCHULZ, NICHOLAS,
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: 17YROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSS:
ADDRESSSE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 1891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
8.1%; Score 74; DB 2
Best Local Similarity 27.0%; Pred. No. 8.3;
Matches 38; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/CDOCKET NUMBER: 2026-4105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
            APPLICATION NUMBER: US/08/804,227C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
     APPLICALL...
FILING DATE: February ---
CLASSIFICATION: 435
TATORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-823
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-776-2459
: INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
TENGTH: 1891 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 8, Application US/08673789
; Patent No. 5814479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1298 DRASVVG--LLGVVEGLGVPL 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 -- SAMMGGILLALIEGVGILL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide US-08-804-227C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10154
                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-673-789-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1107 WRRVVGVVAGGGEDQVAVRGGGVF----GRRLVGVGV----RGGSCVWRAR-----GCVV 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1154 VTGGL-GGVGGHVARWLARSGAEHVVLAGRRGGGVVGAVELERELVGLGAKVTFVSCDVG 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 VWGGLFXTIDCGLVRLRGKEDPWNSITSGALIGAVLAARSGPLAMVG------ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 WRIVDDC---GGAFTMGVIGGGVFQAIKGFRNAPVGIRHRLRGSANAVRIRAPQIGGSFA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

8.6%; Score 78; DB 2; Length 1580;
Best Local Similarity 27.7%; Pred. No. 2.2;
Matches 39; Conservative 18; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-804-227C-12
Sequence 12, Application US/08804227C
Sequence 12, Application US/08804227C
Sequence 12, Application US/08804227C
SENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kubactoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
ITILE OF INVENTION: POLYKETIDE SYNTHASE GENES
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
                                                                                                                                                                                                                                                                                      SCHWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: FEDENBAT 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G
REGISTRATION NUMBER: 35,784
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1980 amino acids
TYPE: amino acids
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOWAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: LILLY CORPORATE CENTER CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1213 DRASMVG--LLGVVEGLGVPL 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 --SAMMGGILLALIEGVGILL 133
                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-08-804-227C-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                    46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

```
471 VTYRKKGDSNSYNVRRTE-----GFSVTLDDLAPDTTYLVQVQALTQEGQGAGSKV 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 LTGAVLAAR-SGPLANVGSANMGGILLALIEGVGILL-TRYTAQQFRNAPP--FLEDPSQ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 IRHRLRGSANAVRIRAPQIGGSFAVWGGLFXTID-----CGLVRLRGKEDPWNSIISGA 97
                                                                                                                                        662 KYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAAAAGFGLVGAAGLGGL--- 719
                                                                                                                    69 -WGGLFXIIDCGLVRLRGKEDPWNSITSG---ALTGAVLAARSGPLAMVGSANMGGILLA 124
                                              24 GVIGGGVFQAIKGF-RNAPVGIRHRL-----RGSANAVR-----IRAPQIGGSFAV---- 69
                                                                                 602 GVPGLGVGAGGVPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAARAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 976;
                                                                                                                                                                                                                                                                                                              RESULT

Sequence 18, Application PC/TUS9504681

Sequence 18, Application PC/TUS9504681

Sequence 18, Application PC/TUS9504681

GENERAL INFORMATION:
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 72.5;
Pred. No. 4.9
 27.0%; Pred. No. 3.7;
tive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-08-804-227C-4
; Sequence 4, Application US/08804227C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%;
23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 976 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                     34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 29; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                        125 LIEGVG 130
                                                                                                                                                                                                                                719 ---GVG 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 LPP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKP 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Morris, Colleen A.
TITLE OF INVENTION: Diagnosis of Williams Syndrome and
TITLE OF INVENTION: Williams Syndrome Cognitive Profile by Analysis of the
TITLE OF INVENTION: Williams Syndrome Cognitive Profile by Analysis of the
TITLE OF INVENTION: Presence or Absence of a LIM-Kinase Gene
                                                                                                                                                                                                                                                   ς.
Σ
                                                                                                                                                                                                                                                                                                                                                            98 LIGAVLAAR-SGPLAMVGSAMMGGILLALIEGVGILL-TRYTAQQFRNAPP--FLEDPSQ 153
                                                                                                                                                                                                                                                                                                                                                                                      44 IRHRLRGSANAVRIRAPQIGGSFAVWGGLFXTID-----CGLVRLRGKEDPWNSITSGA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 792;
                                                                                                                                                                                                                  DB 2; Length 977;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C. STREET: 555 Thirteenth Street, N.W., Suite 701 East STREET: Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                      Query Match
8.0%; Score 72.5; E
Best Local Similarity 23.6%; Pred. No. 4.9;
Matches 29; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.0%; Score 72.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7 1984-40 US-08-678-0398-40 Sequence 40, Application US/086780398 Patent No. 5858662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-624-1589
TELEFAX: 202-783-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Stephen A.
REGISTRATION NUMBER: 38.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 792 amino acids amino acid
                   TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-678-039A-40
                                                                                                           TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
US-08-673-789-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: DC
COUNTRY: U.:
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                154 LPP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     583 LKP 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                         g
```

ŝ

Gaps

```
73 --FXTIDCGLVRLRGKEDPWNSIT-SGALT-----GAVLAARSGPLAMVGSAMMGGIL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 LALIEGVGILL--TRYTAQQFRNAPPFLE---DPSQLPPKDG-------TPAPGYPSY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 ----EGVTVLSLPTSYDVGYVRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADNYQFS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 TMGVIGGGVFQAIKGFRNAPVGIRHRLRGSAN----AVRIRAPQIGGSFAVWGGL---- 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/08466033
Patent No. 5766840
GENERAL INFORMATION:
APPLICANT: Wages, John
APPLICANT: Wangs, John
APPLICANT: Linnen, LaVonne M.
APPLICANT: Linnen, Jeffrey M.
TITLE OF INVENTION: Hepatitis G Virus and Molecular
TITLE OF INVENTION: Cloning Thereof
                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/No/21f ----
FILLING NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.8%; Score 71.5; DB 1; Best Local Similarity 22.4%; Pred. No. 2.4; Matches 41; Conservative 26; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 2747-054-27 CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                     US/08/216,276A
23-MAR-1994
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELES: 248855 OPAT UR
INFORMATION FOR SEO ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 484 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
Virginia
                                        22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 QQY 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 SQY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-216-276A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-466-033-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDD
TILLE OF INVENTION: SPECIFIC DNA AND RNA SEQUENCES
TITLE OF INVENTION: ASSOCIATED WITH US IBDV VARIANTS, VECTOR CARRYING DNA
TITLE OF INVENTION: SEQUENCES, HOST CARRYING CLONED VECTOR, DEDUCED AMINO ACID
TITLE OF INVENTION: SEQUENCES, VACCINE AND METHOD OF VACCINATION
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1666 RLRGSRTGVFVGTNGQHYMPLLQNGGDSFDGYLGTGNSASVMSGRLSYVFGLEGPAVTVD 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 SG-----ALTGAVLAARSG--PLAMVGSAMM------G 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 RLRGSANAVRIRAP-----QIGG----SFAVWGGLFXTIDCGLVRLRGKEDPWNSIT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1786 ADGVALGEGVGVLLVERLSDAERNGHPVLAVVRGSAVNODGASNGLTAPNGPSOOR 1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GILLALIEGVGILLTRYTAQQFRNAPPFL----EDPSQLPPKDGTPAPGYPSYQQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.9%; Score 72; DB 2; Length 3729;
25.6%; Pred. No. 36;
Live 16; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                APPLICANT: Deficit, Bradley S.
APPLICANT: Kubstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
HUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM COMPatible
COMPUTER: IBM COMPatible
COMPUTER: ASCI(DOS) Text only
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTONREY, AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: X-8231
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/08216276A Patent No. 5595912 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3729 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.6%
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-804-227C-4
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington
                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                     46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-216-276A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
107 SGPLAMVGSAMMGGILLALIEGVGILLTRYT----AQQFRNAPPFLEDP-SQLPPKDGT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 2873;
73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94306
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/638,911A
FILING DATE: 04/24/96
CLASSIFICATION: 435
                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/638,911A
FILING DATE: 04/24/96
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/08638911A
Patent No. 5766916
GENERAL INFORMATION:
APPLICANT: Belaeyv, Alexander S.
APPLICANT: Chong, Susan M.
TITLE OF INVENTION: Hepatitis G Virus Protease
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 4600-0124
REFERENCE/CDCKET NUMBER: 4600-0124
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTER/STICS:
LENGTH: 2873 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.5%; Score 68; Best Local Similarity 29.5%; Pred. No. 7 Matches 18; Conservative 13; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-638-911A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-08-638-911A-25
                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                   STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1613 P 1613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 P 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ς,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1553 AGPILMIGLAIAGGMIYASYTGSLVVVTDWDVKGGGAPLYRHGDQATPQPVVQVPPVDHR 1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 SGPLAMVGSAMMGGILLALIEGVGILLTRYT----AQQFRNAPPFLEDP-SQLPPKDGT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.5%; Score 68; DB 2; Length 2873; Best Local Similarity 29.5%; Pred. No. 73; Matches 18; Conservative 13; Mismatches 24; Indels
                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE TO THE TOTAL OF THE TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX. (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2873 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis G Virus Protease
       : Dehlinger & Associates
350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/389,886
FILING DATE: 15-FEB-1995
FILING DATE: 16-DEC-1994
PRIOR APPLICATION NUMBER: US 08/329,729
FILING DATE: 26-OCT-1994
PRIOR APPLICATION NUMBER: US 08/344,271
FILING DATE: 23-NOV-1994
PRIOR APPLICATION NUMBER: US 08/285,588
FILING DATE: 03-AGC-1994
PRIOR APPLICATION NUMBER: US 08/285,543
FILING DATE: 03-AGC-1994
PRIOR APPLICATION NUMBER: US 08/285,543
FILING DATE: 03-AGC-1994
PRIOR APPLICATION NUMBER: US 08/246,985
FILING DATE: 30-MAY:
ATTORNEY AGENT INFORMATION:
NAME: Fablan, GATY R.
REGISTRATION NUMBER: 33,875
PREDEDENEY POOCET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-638-911A-2
Sequence 2, Application US/08638911A
Patent No. 5766916
GENERAL INFORMATION:
APPLICANT: Belaeyv, Alexander S.
APPLICANT: Chong, Susan M.
TITLE OF INVENTION: Hepatitis G V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                        ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                     STREET: 330 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                   USA
                                                                                                                                                                                                                                                                                                         FILING DATE
       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1613 P 1613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 P 161
                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

```
COUNTRY: US
ZIP: 94306
                                                                                                                                                                           US-08-638-911A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-638-911A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P 808
                                                              161 P 161
                                                                                               808 P 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 P 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    808
                                                                                                                                                        RESULT
                                                              òλ
                                                                                             g
                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                            107 SGPLAMVGSAMMGGILLALIEGVGILLTRYT----AQQFRNAPPFLEDP-SQLPPKDGT 160
                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                   Query Match 7.5%; Score 68; DB 2; Length 853; Best Local Similarity 29.5%; Pred. No. 14; Matches 18; Conservative 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.5%; Score 68; DB 2; Length 853; Best Local Similarity 29.5%; Pred. No. 14; Matches 18; Conservative 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
JURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/638,911A
FILING DATE: 04/24/96
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Belaeyv, Alexander S.
APPLICANT: Chong, Susan M.
ITILE OF INVENTION: Hepatitis G Virus Protease NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
REGISTRATION NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 4600-0124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 833 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 4600-0124
REFERENCE/DOCKET NUMBER: 4600-0124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0800
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Application US/08638911A Patent No. 5766916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 853 amino acids
amino acid
                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-638-911A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-638-911A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-08-638-911A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                      161 P 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                           808 P 808
                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                 治
```

107 SGPLAMVGSAMMGGILLALIEGVGILLTRYT----AQQFRNAPPFLEDP-SQLPPKDGT 160

à

THIS PAGE BLANK (uspro)